

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
- (ii) TITLE OF INVENTION: DNA MOLECULES AND PROTEIN DISPLAYING
IMPROVED TRIAZINE COMPOUND DEGRADING ABILITY
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
 - (B) STREET: 119 North Fourth Street
 - (C) CITY: Minneapolis
 - (D) STATE: Minnesota
 - (E) COUNTRY: USA
 - (F) ZIP: 55401
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIORITY APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/035,404
 - (B) FILING DATE: 17-JAN-1997
 - (C) CLASSIFICATION:
- (vii) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not Assigned
 - (B) FILING DATE: 16-JAN-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MCCORMACK, MYRA M.
 - (B) REGISTRATION NUMBER: 36,602
 - (C) REFERENCE/DOCKET NUMBER: 110.00400201
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-305-1225
 - (B) TELEFAX: 612-305-1228

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCGA GCATGGTGAC 60

CTTGACGCCG CTCTTTTCGT TCTCTTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT 120

GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT 180

TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA 240

AACGCTCAGC ATCCAGCACG GTACCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG 300

GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC 360

GGTGCCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCGGC AAGGTCGTGT TACCCGGTTT 420

CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG 480

TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCGA TGAGACCGGA 540

GGACGTAGCG GTGGCGGTGA GGTGTGATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC 600

GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT 660

CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTTGATC GGATGGACGG 720

GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAGTCG AACTGTGCTC 780

GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA 840

TGGCACGGCA GGAGGTCGTA TATCAGTTTG GCCCGCTCCT GCCACTACCA CGGCGGTGAC 900

AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT 960

TCACATGGCG GAGAGCGATC ATGATGAGCG GATTCATGGG ATGAGTCCCG CCGAGTACAT 1020

GGAGTGTTAC GGACTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG 1080

GAAGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA 1140

TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT 1200

GGGCATTGGA ACAGATAACG GGAATAGTAA TGACTCCGCA AACATGATCG GAGACATGAA 1260

GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA 1320

GATTCTTGAA ATGGCGACGA TCGATGGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG 1380
 TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG 1440
 ACTCTCACAT CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500
 TGTCTTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560
 ACGTGAGTTG GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC 1620
 GAACATGGTG GCTAACCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680
 GCCGCCCCCTT GAGGAAATCG CTGCCATCTT GGCGCGGCTC GGATTGGGGG GCGGACATGA 1740
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCACCTCCG TCCTTCGCTC GTGTGGAATC 1800
 GTTGGTAGGT GAGGGTCGAC TCGGGCGGCC AGCTTCCCGA AGAGGTGAAA GGCCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5					10					15	
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20					25					30		
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
		35					40						45		
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
		50				55					60				
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
	65				70					75				80	
Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln
			85					90						95	
Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys
			100					105					110		
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp
			115				120					125			

Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly
130						135					140				
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met
145					150					155					160
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro
				165					170					175	
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp
			180					185					190		
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg
		195					200					205			
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu
	210					215					220				
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp
225					230					235					240
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met
				245					250					255	
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu
			260					265					270		
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu
		275					280					285			
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr
	290					295					300				
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met
305					310					315					320
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Ala	Asn
				325					330					335	
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His
			340					345					350		
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr
		355					360					365			
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile
	370					375					380				
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Leu
385					390					395					400
Arg	Arg	Leu	Ser	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala	Tyr
				405					410					415	
Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met	Glu
			420					425					430		

Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu
 435 440 445

Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met
 450 455 460

Val Ala Asn Pro Ala Trp Arg Ser Leu
 465 470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGAGCATGG	TGACCTTGAC	GCCGCTCTTT	TCGTTCTCTT	TGTTGAACTG	CACGCGAAAG	60
GCTTCCAGGT	CGGTGATGTC	CGCGTCGTCG	TGGTTGGTGA	CGTGCGGGAT	GACCACCCAG	120
TTGCGGTGCA	GGTTTTTCGA	TGGCATAATA	TCTGCGTTGC	GACGTGTAAC	AACTATTGG	180
AGACATATCA	TGCAAACGCT	CAGCATCCAG	CACGGTACCC	TCGTCACGAT	GGATCAGTAC	240
CGCAGAGTCC	TTGGGGATAG	CTGGGTTTAC	GTGCAGGATG	GACGGATCGT	CGCGCTCGGA	300
GTGCACGCCG	AGTCGGTGCC	TCCGCCAGCG	GATCGGGTGA	TCGATGCACG	CGGCAAGGTC	360
GTGTTACCCG	GTTTCATCAA	TGCCCACACC	CATGTGAACC	AGATCCTCCT	GCGCGGAGGG	420
CCCTCGCACG	GGCGTCAATT	CTATGACTGG	CTGTTCAACG	TTGTGTATCC	GGGACAAAAG	480
GCGATGAGAC	CGGAGGACGT	AGCGGTGGCG	GTGAGGTTGT	ATTGTGCGGA	AGCTGTGCGC	540
AGCGGGATTA	CGACGATCAA	CGAAAACGCC	GATTCGGCCA	TCTACCCAGG	CAACATCGAG	600
GCCGCGATGG	CGGTCTATGG	TGAGGTGGGT	GTGAGGGTCG	TCTACGCCCC	CATGTTCTTT	660
GATCGGATGG	ACGGGCGCAT	TCAAGGGTAT	GTGGACGCCT	TGAAGGCTCG	CTCTCCCCAA	720
GTGAACTGT	GCTCGATCAT	GGAGGGAACG	GCTGTGGCCA	AAGATCGGAT	CACAGCCCTG	780
TCAGATCAGT	ATCATGGCAC	GGCAGGAGGT	CGTATATCAG	TTTGGCCCGC	TCCTGCCACT	840
ACCACGGCGG	TGACAGTTGA	AGGAATGCGA	TGGGCACAAG	CCTTCGCCCC	TGATCGGGCG	900
GTAATGTGGA	CGCTTCACAT	GGCGGAGAGC	GATCATGATG	AGCGGATTCA	TGGGATGAGT	960

CCCGCCGAGT ACATGGAGTG TTACGGACTC TTGGATGAGC GTCTGCAGGT CGCGCATTGC 1020
 GTGTACTTTG ACCGGAAGGA TGTTTCGGCTG CTGCACCGCC ACAATGTGAA GGTTCGCGTCG 1080
 CAGGTTGTGA GCAATGCCTA CCTCGGCTCA GGGGTGGCCC CCGTGCCAGA GATGGTGGAG 1140
 CGCGGCATGG CCGTGGGCAT TGGAACAGAT AACGGGAATA GTAATGACTC CGTAAACATG 1200
 ATCGGAGACA TGAAGTTTAT GGCCCATATT CACCGCGCGG TGCATCGGGA TCGGGACGTG 1260
 CTGACCCCAG AGAAGATTCT TGAAATGGCG ACGATCGATG GGGCGCGTTC GTTGGGAATG 1320
 GACCACGAGA TTGGTTCCAT CGAAACCGGC AAGCGCGCGG ACCTTATCCT GCTTGACCTG 1380
 CGTCACCCTC AGACGACTCC TCACCATCAT TTGGCGGCCA CGATCGTGTT TCAGGCTTAC 1440
 GGCAATGAGG TGGACACTGT CCTGATTGAC GGAAACGTTG TGATGGAGAA CCGCCGCTTG 1500
 AGCTTTCTTC CCCCTGAACG TGAGTTGGCG TTCCTTGAGG AAGCGCAGAG CCGCGCCACA 1560
 GCTATTTTGC AGCGGGCGAA CATGGTGGCT AACCAGCTT GGCGCAGCCT CTAGGAAATG 1620
 ACGCCGTTGC TGCATCCGCC GCCCCTTGAG GAAATCGCTG CCATCTTGGC GCGGCTCGGA 1680
 TTGGGGGGCG GACATGACCT TGATGGATAC AGAATTGCCA TGAATGCGGC ACTTCCGTCC 1740
 TTCGCTCGTG TGGAATCGTT GGTAGGTGAG GGTGCGACTG GGGCGCCAGC TTCCCGAAGA 1800
 AGTGAAAG 1808

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGCGCCGCC ACAGCAGCCT TGATCATGAA GCGGAGCATG GTGACCTTGA CGCCGCTCTT 60
 TTCGTTCTCT TTGTTGAACT GCACGCGAAA GGCTTCCAGG TCGGTGATGT CCGCGTCGTC 120
 TGGGTTGGTG ACGTGCAGGA TGACCACCCA GTTGCGGTGC AGGTTTTTTCG ATGGCGTAAT 180
 ATCTGCGTTG CGACGTGTAA CACACTATTG GAGACATATC ATGCAAACGC TCAGCATCCA 240
 GCACGGTACC CTCGTCACGA TGGATCAGTA CCGCAGAGTC CTTGGGGATA GCTGGGTTCA 300
 CGTGCAGGAT GGACGGATCG TCGCGCTCGG AGTGCACGCC GAGTCGGTGC CTCCGCCAGC 360

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 601 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala	Ser	Met	Val	Thr	Leu	Thr	Pro	Leu	Phe	Ser	Phe	Ser	Leu	Leu	Asn
1				5					10					15	
Cys	Thr	Arg	Lys	Ala	Ser	Arg	Ser	Val	Met	Ser	Ala	Ser	Ser	Trp	Leu
			20					25					30		
Val	Thr	Cys	Gly	Met	Thr	Thr	Gln	Leu	Arg	Cys	Arg	Phe	Phe	Asp	Gly
		35					40					45			
Ile	Ile	Ser	Ala	Leu	Arg	Arg	Val	Thr	His	Tyr	Trp	Arg	His	Ile	Met
	50					55					60				
Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln	Tyr
65					70					75					80
Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg	Ile
				85					90					95	
Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp	Arg
			100					105					110		
Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn	Ala
		115					120					125			
His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His	Gly
	130					135					140				
Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln	Lys
145					150					155					160
Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys	Ala
				165					170					175	
Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp	Ser
			180					185					190		
Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	Glu
		195					200					205			
Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	Asp
	210					215					220				
Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	Gln
225					230					235					240
Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Gly	Thr	Ala	Val	Ala	Lys	Asp	Arg
				245					250					255	

Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	Ile	
			260						265						270	
Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	Gly	
		275					280					285				
Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	Thr	
		290				295					300					
Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met	Ser	
305					310					315					320	
Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu	Gln	
				325				330						335		
Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	His	
			340				345						350			
Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	Leu	
		355					360					365				
Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	Ala	
	370					375					380					
Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	Met	
385					390					395				400		
Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	Arg	
				405					410					415		
Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	Ile	
			420					425					430			
Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	Glu	
		435					440					445				
Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	Gln	
	450					455					460					
Thr	Thr	Pro	His	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala	Tyr	
465					470					475					480	
Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met	Glu	
				485					490					495		
Asn	Arg	Arg	Leu	Ser	Phe	Leu	Pro	Pro	Glu	Arg	Glu	Leu	Ala	Phe	Leu	
			500					505					510			
Glu	Glu	Ala	Gln	Ser	Arg	Ala	Thr	Ala	Ile	Leu	Gln	Arg	Ala	Asn	Met	
		515					520					525				
Val	Ala	Asn	Pro	Ala	Trp	Arg	Ser	Leu	Glu	Met	Thr	Pro	Leu	Leu	His	
	530					535					540					
Pro	Pro	Pro	Leu	Glu	Glu	Ile	Ala	Ala	Ile	Leu	Ala	Arg	Leu	Gly	Leu	
545					550					555					560	

Leu Phe Asn Val Val Tyr Pro Gly Gln Lys Ala Met Arg Pro Glu Asp
165 170 175

Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys	Ala	Glu	Ala	Val	Arg	Ser	Gly	
			180					185					190			
Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp	Ser	Ala	Ile	Tyr	Pro	Gly	Asn	
		195					200					205				
Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	Glu	Val	Gly	Val	Arg	Val	Val	
	210					215					220					
Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	Asp	Gly	Arg	Ile	Gln	Gly	Tyr	
225					230					235					240	
Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	Gln	Val	Glu	Leu	Cys	Ser	Ile	
				245					250					255		
Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp	Arg	Ile	Thr	Ala	Leu	Ser	Asp	
			260					265					270			
Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	Ile	Ser	Val	Trp	Pro	Ala	Pro	
		275					280					285				
Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	Gly	Met	Arg	Trp	Ala	Gln	Ala	
	290					295						300				
Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	Thr	Leu	His	Met	Ala	Glu	Ser	
305					310					315					320	
Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met	Ser	Pro	Ala	Asp	Tyr	Met	Glu	
				325					330					335		
Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu	Gln	Val	Ala	His	Cys	Val	Tyr	
			340					345					350			
Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	His	Arg	His	Asn	Val	Lys	Val	
		355					360					365				
Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	Leu	Gly	Ser	Gly	Val	Ala	Pro	
	370					375					380					
Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	Ala	Val	Gly	Ile	Gly	Thr	Asp	
385					390					395					400	
Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	Met	Ile	Gly	Asp	Met	Lys	Phe	
				405					410					415		
Met	Ala	His	Ile	His	Arg	Ala	Val	His	Arg	Asp	Ala	Asp	Val	Leu	Thr	
			420					425					430			
Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	Ile	Asp	Gly	Ala	Arg	Ser	Leu	
		435					440					445				
Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	Glu	Thr	Gly	Lys	Arg	Ala	Asp	
	450					455					460					

Leu Ile Leu Leu Asp Leu Arg His Pro Gln Thr Thr Pro His His His
 465 470 475 480
 Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr Gly Asn Glu Val Asp Thr
 485 490 495
 Val Leu Ile Asp Gly Asn Val Val Met Glu Asn Arg Arg Leu Ser Phe
 500 505 510
 Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu Glu Glu Ala Gln Ser Arg
 515 520 525
 Ala Thr Ala Ile Leu Gln Arg Ala Asn Met Val Ala Asn Pro Ala Trp
 530 535 540
 Arg Ser Leu Glu Met Thr Pro Leu Leu His Pro Pro Pro Leu Glu Glu
 545 550 555 560
 Ile Ala Ala Ile Leu Ala Arg Leu Gly Leu Gly Gly Gly His Asp Leu
 565 570 575
 Asp Gly Tyr Arg Ile Ala Met Asn Ala Ala Leu Pro Ser Phe Ala Arg
 580 585 590
 Val Glu Ser Leu Val Gly Glu Gly Arg Leu Arg Ala Pro Ala Ser Arg
 595 600 605
 Arg Ser Glu Arg Pro Glu
 610

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGTATCGGG GAATTCCTGA GCGCGGCCAC AGCAGCCNTG ATCATGAAGG CGAGCATGGT 60
 GACCTNGACG CCGTNTTTTNN GTTNTTTTTTT GTTGAAGTGC ACGCGAAAGG TTCCAGGTGC 120
 GTGATGTCCG CGTCGTCGTG GTTGGTGACG TGCGGGATGA CCACCCAGNT GCGGTGCAGG 180
 TTTTTCGATG GCATAATATC TCGTTGCGA CGTGTAACAC ACTANTGGAG ACATATCATG 240
 CAAACGCTCA GCATCCAGCA CGGTACCCTC GTCACGATGG ATCAGTACCG CAGAGTCCTT 300
 GGGGATAGCT GGGTTCACGT GCAGGATGGA CGGATCGTCG CGCTCGGAGT GCACGCCGAG 360

TCGGTGCCTC CGCCAGCGGA TCGGGTGATC GATGCACGCG GCAAGGTCGT GTTACCCGGT 420
 TTCATCAATG CCCACACCCA TGTGAACCAG ATCCTCCTGC GCGGAGGGCC CTCGCACGGG 480
 CGTCAATTCT ATGACTGGCT GTTCAACGTT GTGTATCCGG GACAAAAGGC GATGAGACCG 540
 GAGGA 545

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCTGCGCGGA GGGCCTCCGC ACGGGCGTCA ATTCTATGAC TGGCTGTTCA ACGTTGTGTA 60
 TCCGGGACAA AAGGCGATGA GACCGGAGGA CGTAGCGGTG GCGGTGAGGT TGTATTGTGC 120
 GGAAGCTGTG CGCAGCGGGA TTACGACGAT CAACGAAAAC GCCGATTCGG CCATCTACCC 180
 AGGCAACATC GAGGCCGCGA TGGCGGTCTA TGGTGAGGTG GGTGTGAGGG TCGTCTACGC 240
 CCGCATGTTT TTTGATCGGA TGGACGGGCG CATTCAAGGG TATGTGGACG CCTTGAAGGC 300
 TCGCTCTCCC CAAGTCGAAC TGTGCTCGAT CATGGAGGAA ACGGCTGTGG CCAAAGATCG 360
 GATCACAGCC CTGTCAGATC AGTATCATGG CACGGCAGGA GGTCCTATAT CAGTTTGGCC 420
 CGCTCCTGCC ACTACCACGG CGGTGACATT TAAANGAATC CATGGGCCAA CCTCCCCCGT 480
 GATCCGGCGG TAATGTGAC 499

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TNGCAGGTTG TGAGCATGCT ACTTCGGTTC AGNGTGGCC CCCGTGCCAG AGATGGTGGA 60
 GCGCGGCATG GCCGTGGGCA TTGGAACAGA TAACGGGAAT AGTAATGACT CCGTAAACAT 120
 GATCGGAGAC ATGAAGTTTA TGGCCCATAT TCACCGCGCG GTGCATCGGG ATGCGGACGT 180
 GCTGACCCCA GAGAAGATTN TTGAAATGGC GACGATCGAT GGGGCGCGTT TCGTTGGGGA 240
 TGGACCACGA GATTGGTTCC ATCGAAACCG GCAAGCGCGC GGACCTTATC CTGCTTGACC 300
 TCGGTCACCC TCAGACGACT CCTCACCATC ATTTGGCGGC CACGATCGTG TTTCAGGCTT 360

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGCCACGAT CGTGTTTCAG GCTTACGGCA ATGAGGTGGA CACTGTCCTG ATTGACGGAA 60
 ACGTTGTGAT GGAGAACCGC CGCTTGAGCT TTCTTCCCCC TGAACGTGAG TTGGCGTTCC 120
 TTGAGGAAGC GCAGAGCCGC GCCACAGCTA TTTTGCATCG GCGGAAACAT GGTGGCTAAC 180
 CCAGCTTGGC GCAGCCTCTA GGAAATGACG CCGTTGCTGC ATCCGCCGCC CCTTGAGGAA 240
 ATCGCTGCCA TCTTGGCGCG GCTCGGATTG GGGGGCGGAC ATGACCTTGA TGGATACAGA 300
 ATTGCCATGA ATGCGGCACT TCCGTCCTTC GCTCGTGTGG AATCGTTGGT AGGTGAGGGT 360
 CGACTGCGGG CGCCAGCTTC CCGAAGAGGT GAAAGCCCGA GGATCCTCTA GAGTCCGATT 420
 TTTCCGATGT CATCACCGGC GCG 443

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGCGCGGA GGCCTCCGCA CGGGCGTCAA TTCTATGACT GGCTGTTCAA CGTTGTGTAT 60
 CCGGGACAAA AGGCGATGAG ACCGGAGGAC GTANCGGTGG CCGTGAGGTT GTATTGTGCG 120
 GAAGCTGTGC GCAGCGGGAT TACGACGATC AACGAAAACG CCGATTCTGGC CATCTACCCA 180
 GGCAACATCG AGGCCGCGAT GCGGGTCTAT GGTGAGGTGG GTGTGAGGGT CGTCTACGCC 240
 CGCATGTTCT TTGATCGGAT GGACGGGCGC ATTCAAGGGT ATGTGGACGC CTTGAAGGCT 300
 CGCTCTCCCC AAGTCGAACT GTGCTCGATC ATGGAGGAAA CGGCTGTGGC CAAAGATCGG 360
 ATCACANCCC TGTCAGATCA NTATCATGGC ACGGCANGAG GTCCTATATC ANTTTGGCCC 420
 GCTCCTGCCA CTACCACNGC GGTGACATTT NAANGAATTC CATNGGCACA ACCTTCCCCC 480
 GTGATCNGGC GGTAATGTNG ACCCA 505

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Pro His Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Leu Tyr Pro
 1 5 10 15
 Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
 20 25 30
 Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
 35 40 45
 Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val
 50 55 60
 Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp
 65 70 75 80
 Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg
 85 90 95
 Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala
 100 105 110

Lys Asp Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly
 115 120 125

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
 130 135 140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser His Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Leu Tyr Pro
 1 5 10 15

Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
 20 25 30

Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
 35 40 45

Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val
 50 55 60

Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp
 65 70 75 80

Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Thr Leu Lys Ala Arg
 85 90 95

Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala
 100 105 110

Lys Asp Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly
 115 120 125

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
 130 135 140

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro	His	Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	1	5	10	15
Gly	Gln	Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	20	25	30	
Tyr	Cys	Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	35	40	45	
Ala	Asp	Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	50	55	60	
Tyr	Gly	Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	65	70	75	80
Arg	Met	Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	85	90	95	
Ser	Pro	Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	100	105	110	
Lys	Asp	Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	115	120	125	
Gly	Arg	Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	130	135	140	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser	His	Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Leu	Tyr	Pro	1	5	10	15
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(2) INFORMATION FOR SEQ ID NO:16:

(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	His	Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro
1				5					10					15	
Gly	Gln	Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu
			20					25					30		
Tyr	Cys	Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn
		35					40					45			
Ala	Asp	Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val
	50					55					60				
Tyr	Gly	Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp
65					70					75					80

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
130 135 140

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

CGCGAAAGGC	TTCCAGGTCG	GTGATGTCCG	CGTCGTCTGT	GTTGGTGACG	TGCGGGATGA	60
CCACCCAGTC	GCGGTGCAGG	TTTTTCGATG	GCATAATATC	TGCGTTGCGA	CGTGTAACAC	120
ACTATTGGAG	ACATATCATG	CAAACGCTCA	GCATCCAGCA	CGGTACCCTC	GTCACGATGG	180
ATCAATACCG	CAGAGTCCTT	GGGGATAGCT	GGGTTTACGT	GCAGGATGGA	CGGATCGTCG	240
CGCTCGGAGT	GCACGCCAAG	TCGGTGCCTC	CGCCAGCGGA	TCGGGTGATC	GATGCACGCG	300
GCAAGGTCGT	GTTACCCGGT	TTCATCAATG	CCCACACCCA	TGTGAACCAG	ATCCTCCTGC	360
GCGGAGGGCC	CTCGCACGGG	CGTCAATTCT	ATGACTGGCT	GTTCAACGTT	GTGTATCCGG	420
GACAAAAGGC	GATGAGACCG	GAGGACGTAG	CGGTGGCGGT	GAGGTTGTAT	TGTGCGGAAG	480
CTGTGCGCAG	CGGGATTACG	ACGATCAACG	AAAACGCCGA	TTCGGCCATC	TACCCAGGCA	540
ACATCGAGGC	CGCGATGGCG	GTCTATGGTG	AGGTGGGTGT	GAGGGTCGTC	TACGCCCCGA	600
TGTTCTTTGA	TCGGATGGAC	GGGCGCATT	AAGGGTATGT	GGACGCCTTG	AAGGCTCGCT	660
CTCCCCAAGT	CGAACTGTGC	TCGATCATGG	AGGAAACGGC	TGTGGCCAAA	GATCGGATCA	720
CAGCCCTGTC	AGATCAGTAT	CATGGCACGG	CAGGAGGTCG	TATATCAGTT	TGGCCCGCTC	780
CTGCCACTAC	CACGGCGGTG	ACAGTTGAAG	GAATGCGATG	GGCACAAGCC	TTCGCCCGTG	840

ATCGGGCGGT AATGTGGACG CTTACATGG CGGAGAGCGA TCATGATGGG CGGATTCATG 900
 GGATGAGTCC CGCCGAGTAC ATGGAGTGTT ACGGACTCTT GGATGAGCGT CTGCAGGTCC 960
 CGCATTGCGT GTACTTTGAC CGGAAGGATG TTCGGCTGCT GCACCGCCAC AATGTGAAGG 1020
 TCGCGTCGCA GGTGTGTAGC AATGCCTACC TCGGCTCAGG GGTGGCCCCC GTGCCAGAGA 1080
 TGGTGGAGCG CGGCATGGCC GTGGGCATTG GAACAGATAA CGGGAATAGT AATGACTCCG 1140
 TAAACATGAT CGGAGACATG AAGTTTATGG CCCATATTCA CCGCGCGGTG CATCGGGATG 1200
 CGGACGTGCT GACCCCAGAG AAGATTCTTG AAATGGCGAC GATCGATGGG GCGCGTTCGT 1260
 TGGGGATGGA CCACGAGATT GGTTCATCG AAACCGGCAA GCGCGCGGAC CTTATCCTGC 1320
 TTGACCTGCG TCACCCTCAG ACGACTCCTC ACCATCATTT GGCGGCCACG ATCGTGTTTC 1380
 AGGCTTACGG CAATGAAGTG GACACTGTCC TGATTGACGG AAACGTTGTG ATGGAGAACC 1440
 GCTGCTTGAG CTTTCTTCCC CCTGAACGTG AGTTGGCGTT CTTGAGGGA GCGCAGAGCC 1500
 GCGCCACAGC TATTTTGCAG CGGGCGAACA TGGTGGCTAA CCCAGCTTGG CGCAGCCTCT 1560
 AGGAAATGAC GCCGTTGCTG CATCCGCCGC CCCTTGAGGA AATCGCTGCC ATCTTGGCGC 1620
 GGCTCGGATT GGG 1633

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGTGGTTGG TGACGTGCGG GATGACCACC CAGTCGCGGT GCAGGTTTTT CGATGGCATA 60
 ATATCTGCGT TGCACGTGT AACACACTAT TGGAGACATA TCATGCAAAC GCTCAGCATC 120
 CAGCACGGTA CCCTCGTCAC GATGGATCAG TACCGCAGAG TCCTTGGGGA TAGCTGGGTT 180
 CACGTGCAGG ATGGACGGAT CGTCGCGCTC GGAGTGCACG CCGAGTCGGT GCCTCCGCCA 240
 GCGGATCGGG TGATCGATGC ACGCGGCAAG GTCGTGTTAC CCGGTTTCAT CAATGCCAC 300
 ACCCATGTGA ACCAGATCCT CCTGCGCGGA GGGCCCTCGC ACGGGCGTCA ATTCTATGAC 360
 TGGCTGTTCA ACGTTGTGTA TCCGGGACAA AAGCGCATGA GACCGGAGGA CGTAGCGGTG 420

GCGGTGAGGT TGTATTGTGC GGAAGCTGTG CGCAGCGGGA TTACGACGAT CAACGAAAAC 480
 GCCGATTTCG CCATCTACCC AGGCAACATC GAGGCCGCGA TGGCGGTCTA TGGTGAGGTG 540
 GGTGTGAGGG TCGTCTACGC CCGCATGTTC TTTGATCGGA TGGACGGGCG CATTCAAGGG 600
 TATGTGGACG CCTTGAAGGC TCGCTCTCCC CAAGTCGAAC TGTGCTCGAT CATGGAGGAA 660
 ACGGCTGTGG CCAAAGATCG GATCACAGCC CTGTCTAGATC AGTATCATGG CACGGCAGGA 720
 GGTCTGATAT CAGTTTGGCC CGCTCCTGCC ACTACCACGG CGGTGACAGT TGAAGGAATG 780
 CGATGGGCAC AAGCCTTCGC CCGTGATCGG GCGGTAATGT GGACGCTTCA CATGGCGGAG 840
 AGCGATCATG ATGAGCGGAT TCATGGGATG AGTCCCGCCG AGTACATGGA GTGTCACGGA 900
 CTCTTGGATG AGCGTCTGCA GGTCGCGCAT TGCCTGTACT TTGACCGGAA GGATGTTTCG 960
 CTGCTGCACC GCCACAATGT GAAGGTCGCG TCGCAGGTTG TGAGCAATGC CTACCTCGGC 1020
 TCAGGGGTGG CCCCCGTGCC AGAGATGGTG GAGCGCGGCA TGGCCATGGG CATTGGAACA 1080
 GATAACGGGA ATAGTAATGA CTCCGTAAAC ATGATCGGAG ACATGAAGTT TATGGCCCAT 1140
 ATTCACCGCG CGGTGCATCG GGATGCGGAC GTGCTGACCC CAGAGAAGAT TCTTGAAATG 1200
 GCGACGATCG ATGGGGCGCG TTCGTTGGGA ATGGACCACG AGATTGGTTC CATCGAAACC 1260
 GGCAAGCGCG CGGACCTTAT CCTGCTTGAC CTGCGTCACC CTCAGACGAC TCCTCACCAT 1320
 CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC TGTCCTGATT 1380
 GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA ACGTGAGTTG 1440
 GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC GAACATGGTG 1500
 GCTAACCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC GCCGCCCTT 1560
 GAGGAAATCG CTGCCATCTT GGCGCGGCTC GGATTGGG 1598

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACGTGCGGGA TGACCACCCA GTTGCGGTGC AGGTTTTTCG ATGGCGTAAT ATCTGCGTTG 60

CGACGTGTAA CACACTATTG GAGACATATC ATGCAAACGC TCAGCATCCA GCACGGTACC 120
 CTCGTACGA TGGATCAGTA CCGCAGAGTC CTTGGGGATA GCTGGGTTCA CGTGCAGGAT 180
 GGACGGATCG TCGCGCTCGG AGTGCACGCC GAGTCGGTGC CTCCGCCAGC GGATCGGGTG 240
 ATCGATGCAC GCGGCAAGGT CGTGTTACCC GGTTCATCA ATGCCCACAC CCATGTGAAC 300
 CAGATCCTCC TGC CGGAGG GCCCTCGCAC GGGCGTCAAT TCTATGACTG GCTGTTCAAC 360
 GTTGTGTATC CGGGACAAA GCGATGAGA CCTGAGGACG TAGCGGTGGC GGTGAGGTTG 420
 TATTGTGCGG AAGCTGTGCG CAGCGGGATT ACGACGATCA ACGAAAACGC CGATTCCGCC 480
 ATCTACCCAG GCAACATCGA GGCCGCGATG GCGGTCTATG GTGAGGTGGG TGTGAGGGTC 540
 GTCTACGCCC GCATGTTCTT TGATCGGATG GACGGGCGCA TTCAAGGGTA TGTGGACGCC 600
 TTGAAGGCTC GCTCTCCCCA AGTCGAACTG TGCTCGATCA TGGAGGAAAC GGCTGTGGCC 660
 AAAGATCGGA TCACAGCCCT GTCAGATCAG TATCATGGCA CGGCAGGAGG TCGTATATCA 720
 GTTTGGCCCG CTCCTGCCAC TACCACGGCG GTGACAGTTG AAGGAATGCG ATGGGCACAA 780
 GCCTTCGCCC GTGATCGGGC GGTAATGTGG ACGCTTCACA TGGCGGAGAG CGATCATGAT 840
 GAGCGGATTC ATGGGATGAG TCCCGCCGAG TACATGGAGT GTTACGGACT CTTGGATGAG 900
 CGTCTGCAGG TCGCGCATTG CGTGTACTTT GACCGGAAGG ATGTTCCGGCT GCTGCACCGC 960
 CACAATGTGA AGGTCGCGTC GCAGGTTGTG AGCAATGCCT ACCTCGGCTC AGGGGTGGCC 1020
 CCCGTGCCAG AGATGGTGGG GCGCGGCATG GCCGTGGGCA TTGGAACAGA TAACGGGAAT 1080
 AGTAATGACT CCGTAAACAT GATCGGAGAC ATGAAGTTTA TGGCCCATAT TCACCGCGCG 1140
 GTGCATCGGG ATGCGGACGT GCTGACCCCA GAGAAGATTC TTGAAATGGC GACAAATCGAT 1200
 GGGGCGCGTT CGTTGGGAAT GGACCACGAG ATTGGTTCCA TCGAAACCGG CAAGCGCGCG 1260
 GACCTTATCC TGCTTGACCT GCGTCACCCT CAGACGACTC CTCACCATCA TTTGGCGGCC 1320
 ACGATCGTGT TTCAGGCTTA CGGCAATGAG GTGGACACTG TCCTGATTGA CGGAAACGTT 1380
 GTGATGGAGA ACCGCCGCTT GAGCTTTCTT CCCCTGAAC GTGAGTTGGC GTTCCTTGAG 1440
 GAAGCGCAGA GCCGCGCCAC AGCTATTTTG CAGCGGGCGA ACATGGTGGC TAACCCAGCT 1500
 TGGCGCAGCC TCTAGGAAAT GACGCCGTTG CTGCATCCGC TGCCCCTTGA GGAAATCGCT 1560
 GCCATCTTGG CGCGGCTCGG ATTGGG 1586

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1597 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGGTTGGT GACGTGGGGG ATGACCACCC AGTCGCGGTG CAGGTTTTTC GATGGCATAA	60
TATCTGCGTT GCGACGTGTA ACACACTATT GGAGACATAT CATGCAAACG CTCAGCATCC	120
AGCACGGTAC CCTCGTCACG ATGGATCAGT ACCGCAGAGT CCTTGGGGAT AGCTGGGTTC	180
ACGTGCAGGA TGGACGGATC GTCGCGCTCG GAGTGCACGC CGAGTCGGTG CCTCCGCCAG	240
CGGATCAGGT GATCGATGCA CGCGGCAAGG TCGTGTACC CGGTTTCATC AATGCCCACA	300
CCCATGTGAA CCAGATCCTC CTGCGCGGAG GGCCCTCGCA CGGGCGTCAA TTCCATGACT	360
GGCTGTTCAA CGTTGTGTAT CCGGGACAAA AGGCGATGAG ACCGGAGGAC GTAGCGGTGG	420
CGGTGAGGTT GTATTGTGCA GAAGCTGTGC GCAGCGGGAT TACGACGATT AACGAAAACG	480
CCGATTCGGC CATCTACCCA GGCAACATCG AGGCCGCGAT GGCGGTCTAT GGTGAGGTGG	540
GTGTGAGGGT CGTCTACGCC CGCATGTTCT TTGATCGGAT GGACGGGCGC ATTCAAGGGT	600
ATGTGGACGC CTTGAAGGCT CGCTCTCCCC AAGTCGAACT GTGCTCGATC ATGGAGGAAA	660
CGGCTGTGGC CAAAGATCGG ATCACAGCCC TGTCAGATCA GTATCATGGC ACGGCAGGAG	720
GTCGTATATC AGTTTGGCCC GCTCCTGCCA CTACCACGGC GGTGACAGTT GAAGGAATGC	780
GATGGGCACA AGCCTTCGCC CGTGATCGGG CGGTAATGTG GACGCTTCAC ATGGCGGAGA	840
GCGATCATGA TGGGCGGATT CATGGGATGA GTCCCGCCGA GTACATGGAG TGTACGGAC	900
TCTTGATGA GCGTCTGCAG GTCGCGCATT GCGTGTACTT TGACCGGAAG GATGTTCGGC	960
TGCTGCACCG CCACAATGTG AAGGTCGCGT CGCAGGTTGT GAGCAATGCC TACCTCGGCT	1020
CAGGGGTGGC CCCCCTGCCA GAGATGGTGG AGCGCGGCAT GGCCGTGGGC ATTGGAACAG	1080
ATAACGGGAA TAGTAATGAC TCCGTAAACA TGATCGGAGA CATGAAGTTT ATGGCCCATA	1140
TTCACCGCGC GGTGCATCGG GATGCGGACG TGCTGACCCC AGAGAAGATT CTTGAAATGG	1200
CAACGATCGA TGGGGCGCGT TCGTTGGGAA TGGACCACGA GATTGGTTCC ATCGAAACCG	1260
GCAAGCGCGC GGACCTTATC CTGCTTGACC TGCCTCACCC TCAGACGACT CCTCACCATC	1320
ATTTGGCGGC CACGATCGTG TTTCAGGCTT ACGGCAATGA GGTGGACACT GTCCTGATTG	1380

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ACGGAAACGT TGTGATGGAG AACCGCCGCT TGAGCTTTCT TCCCCCTGAA CGTGAGTTGG	1440
CGTTCCTTGA GGAAGCGCAG AGCCGCGCCA CAGCTATTTT GCAGCGGGCG AACATGGTGG	1500
CTAACCCAGC TTGGCGCAGC CTCTAGGAAA TGACGCCGTT GCTGCATCCG CCGCCCCCTTG	1560
AGGAAATCGC TGCCATCTTG GCGCGGCTCG GATTGGG	1597

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGACCTTGA CGCCGCTCTT TTCGTTCTCT TTGTTGAACT GCACGCGAAT GGCTTCCAGT	60
TGCATGATGT CCGCGTCGTC GTGGTTGGTG ACGTGCGGGA TGACCACCCA GTCGCGGTGC	120
AGGTTTTTCG ATGGCATAAT ATCTGCGTTG CGACGTGTAA CACACTATTG GAGACATATC	180
ATGCAAACGC TCAGCATCCA GCACGGTACC CTCGTCACGA TGGATCAGTA CCGCAGAGTC	240
CTTGGGGATA GCTGGGTTCA CGTGCAGGAT GGACGGATCG TCGCGCTCGG AGTGCACGCC	300
GAGTCGGTGC CTCCGCCAGC GGATCGGGTG ATTGATGCAC GCGGCAAGGT CGTGTTACCC	360
GGTTTCATCA ATGCCCACAC CCATGTGAAC CAGATCCTCC TCGCGGAGG CCTCGCACGG	420
GCGTCAATTC TATGACTGGC TGTTCAACGT TGTGTATCCG GGACAAAAGG CGATGAGACC	480
GGAGGACGTA GCGGTGGCGG TGAGGTTGTA TTGTGCGGAA GCTGTGCGCA GCGGGATTAC	540
GACGATCAAC GAAAACGCCG ATTCGGCCAT CTACCCAGGC AACATCGAGG CCGCGATGGC	600
GGTCTATGGT GAGGTGGGTG TGAGGGTCGT CTACGCCCCG ATGTTCTTTG ATCGGATGGA	660
CAGGCGCATT CAAGGGTATG TGGACGCCTT GAAGGCTCGC TCTCCCCAAG TCGAACTGTG	720
CTCGATCATG GAGGAAACGG CTGTGGCCAA AGATCGGATC ACAGCCCTGT CAGATCAGTA	780
TCATGGCAGC GCAGGAGGTC GTATATCAGT TTGGCCCCGT CCTGCCACTA CCACGGCGGT	840
GACAGTTGAA GGAATGCGAT GGGCACAAGC CTTGCCCCGT GATCGGGCGG TAATGTGGAC	900
GCTTCACATG GCGGAGAGCG ATCATGATGA GCGGATTCAT GGGATGAGTC CCGCCGAGTA	960
CATGGAGTGT TACGGACTCT TGGATGAGCG TCTGCAGGTC GCGCATTGCG TGTACTTTGA	1020

102550 000000

(2) INFORMATION FOR SEQ ID NO:22:

(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
85 90 95

Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys	
			100						105						110	
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp	
			115				120					125				
Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	
			130			135					140					
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	
145					150					155					160	
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	
				165					170					175		
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp	
			180					185					190			
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	
			195				200						205			
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	
			210			215					220					
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	
225					230					235					240	
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Gly	Arg	Ile	His	Gly	Met	
				245					250					255		
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu	
			260					265					270			
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	
			275				280					285				
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	
						295					300					
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	
305					310					315					320	
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	
				325					330					335		
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	
			340					345					350			
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	
							360					365				
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	
						375					380					
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	
385					390						395				400	

Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala
 405 410 415

Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met
 420 425 430

Glu Asn Arg Cys Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445

Leu Glu Gly Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn
 450 455 460

Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu
 465 470 475 480

His Pro Pro Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
 1 5 10 15

Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
 20 25 30

Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
 35 40 45

Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
 50 55 60

Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95

Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110

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Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp	
115						120						125				
Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	
130						135						140				
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	
145						150						160				
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	
			165						170			175				
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp	
			180						185			190				
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	
			195			200						205				
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	
210						215						220				
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	
225						230						240				
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met	
			245						250			255				
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	His	Gly	Leu	Leu	Asp	Glu	Arg	Leu	
			260						265			270				
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	
275						280						285				
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	
290						295						300				
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	
305						310						320				
Ala	Met	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	
			325						330			335				
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	
			340						345			350				
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	
			355			360						365				
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	
370						375						380				
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	
385						390						395			400	

Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala
 405 410 415

Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met
 420 425 430

Glu Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445

Leu Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn
 450 455 460

Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu
 465 470 475 480

His Pro Pro Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
 1 5 10 15

Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
 20 25 30

Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
 35 40 45

Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
 50 55 60

Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95

Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110

Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125
 Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140
 Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160
 Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175
 Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190
 Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205
 Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220
 Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240
 Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255
 Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270
 Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285
 His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300
 Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320
 Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Val Asn
 325 330 335
 Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350
 Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365
 Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380
 Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Pro
 385 390 395 400
 Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala
 405 410 415

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Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met
 420 425 430
 Glu Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445
 Leu Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn
 450 455 460
 Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu
 465 470 475 480
 His Pro Leu Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
 1 5 10 15
 Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
 20 25 30
 Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
 35 40 45
 Gln Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
 50 55 60
 Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80
 Gly Arg Gln Phe His Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95
 Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110
 Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125

10550 403300

Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	
130						135					140					
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	
145					150					155					160	
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	
				165					170					175		
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp	
			180					185					190			
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	
		195					200					205				
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	
	210					215					220					
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	
225					230					235					240	
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Gly	Arg	Ile	His	Gly	Met	
				245					250					255		
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu	
			260					265					270			
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	
		275					280					285				
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	
	290					295					300					
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	
305				310						315					320	
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	
				325					330					335		
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	
			340					345					350			
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	
		355					360					365				
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	
	370					375					380					
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	
385					390					395					400	
Gln	Thr	Thr	Pro	His	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala	
				405					410					415		
Tyr	Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met	
			420					425					430			

Glu Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445
 Leu Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn
 450 455 460
 Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu
 465 470 475 480
 His Pro Pro Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
 1 5 10 15
 Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
 20 25 30
 Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
 35 40 45
 Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
 50 55 60
 Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80
 Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95
 Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110
 Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125
 Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140

00550-205500

Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met
145					150					155					160
Asp	Arg	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro
			165						170					175	
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp
			180					185					190		
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg
		195					200					205			
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu
	210					215					220				
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp
225					230					235					240
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met
				245					250					255	
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu
			260					265					270		
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Ile	Arg	Leu	Leu
		275					280					285			
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Ala	Val	Ser	Asn	Ala	Tyr
	290					295					300				
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met
305					310					315					320
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn
				325					330					335	
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His
			340					345					350		
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr
		355					360					365			
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile
	370					375					380				
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro
385					390					395					400
Gln	Thr	Thr	Pro	His	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala
				405					410					415	
Tyr	Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met
			420					425					430		
Glu	Asn	Arg	Arg	Leu	Ser	Phe	Leu	Pro	Pro	Glu	Arg	Glu	Leu	Ala	Phe
		435					440					445			

His Pro Pro Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Gln Leu Gly
485 490 495

[illegible]